

11/30/01
1207

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/825,882

DATE: 11/30/2001
TIME: 12:05:39

Input Set : A:\279152rx.app
Output Set: N:\CRF3\11212001\I825882.raw

ENTERED

8.5

3 <110> APPLICANT: ADLER, JON ELLIOT
5 <120> TITLE OF INVENTION: T2R TASTE RECEPTORS AND GENES ENCODING SAME
7 <130> FILE REFERENCE: 078003/0279152/RXT
9 <140> CURRENT APPLICATION NUMBER: 09/825,882
10 <141> CURRENT FILING DATE: 2001-04-05
12 <150> PRIOR APPLICATION NUMBER: 60/195,532
13 <151> PRIOR FILING DATE: 2000-04-07
15 <150> PRIOR APPLICATION NUMBER: 60/247,014
16 <151> PRIOR FILING DATE: 2000-11-13
18 <160> NUMBER OF SEQ ID NOS: 31
20 <170> SOFTWARE: PatentIn Ver. 2.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 1002
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <400> SEQUENCE: 1
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30 ttttggatg tagtgaagag gcaggcactg agcaacagtg attgtgtgct gctgtgtctc 180
31 agcatcagcc ggctttcct gcatggactg ctgttctga gtgctatcca gcttacccac 240
32 ttccagaagt tgagtgaacc actgaaccac agctaccaag ccatcatcat gctatggatg 300
33 attgcaaacc aagccaaacct ctggcttgct gcctgcctca gcctgcctt ctgctccaag 360
34 ctcatccgtt tctctcacac cttectgatc tgcttggcaa gctgggtctc caggaagatc 420
35 tcccagatgc tcctgggtat tattcttgc tcctgcattc gcactgtcct ctgtgtttgg 480
36 tgcttttta gcagacctca ctgcacagtc acaactgtgc tattcatgaa taacaataca 540
37 aggctcaact ggcagattaa agatctcaat ttattttatt ctttcttctt ctgctatctg 600
38 tggctgtgc ctccttcct attgtttctg gtttcttctg ggatgctgac tgtctccctg 660
39 ggaaggcaca tgaggacaat gaaggcttat accagaaaact ctcgtgaccc cagcctggag 720
40 gcccacatta aagccctcaa gtcctttgtc tccttttct gttttttgt gatatcatcc 780
41 tgtgttgct tcatctctgt gcccctactg attctgtggc ggcacaaaat aggggtgatg 840
42 gtttgtgttggataatggc agcttgcctc tctggcatg cagccatctt gatctcaggc 900
43 aatgccaagt tgaggagagc tgtgtatgacc attctgtctt gggctcagag cagcctgaag 960
44 gtaagagccg accacaaggc agattcccg accactgtgct ga 1002
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48 <211> LENGTH: 333
49 <212> TYPE: PRT
50 <213> ORGANISM: Homo sapiens
52 <400> SEQUENCE: 2
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54 1 5 10 15
55 Thr Phe Leu Phe Ile Ser Val Leu Glu Phe Ala Val Gly Phe Leu Thr
56 20 25 30
57 Asn Ala Phe Val Phe Leu Val Asn Phe Trp Asp Val Val Lys Arg Gln
58 35 40 45
59 Ala Leu Ser Asn Ser Asp Cys Val Leu Leu Cys Leu Ser Ile Ser Arg
60 50 55 60
61 Leu Phe Leu His Gly Leu Leu Phe Leu Ser Ala Ile Gln Leu Thr His
62
63
64
65

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66	65	70	75	80													
68	Phe	Gln	Lys	Leu	Ser	Glu	Pro	Leu	Asn	His	Ser	Tyr	Gln	Ala	Ile	Ile	
69															90	95	
71	Met	Leu	Trp	Met	Ile	Ala	Asn	Gln	Ala	Asn	Leu	Trp	Leu	Ala	Ala	Cys	
72															100	105	110
74	Leu	Ser	Leu	Leu	Tyr	Cys	Ser	Lys	Leu	Ile	Arg	Phe	Ser	His	Thr	Phe	
75															115	120	125
77	Leu	Ile	Cys	Leu	Ala	Ser	Trp	Val	Ser	Arg	Lys	Ile	Ser	Gln	Met	Leu	
78															130	135	140
80	Leu	Gly	Ile	Ile	Leu	Cys	Ser	Cys	Ile	Cys	Thr	Val	Leu	Cys	Val	Trp	
81	145														150	155	160
83	Cys	Phe	Phe	Ser	Arg	Pro	His	Phe	Thr	Val	Thr	Thr	Val	Leu	Phe	Met	
84															165	170	175
86	Asn	Asn	Asn	Thr	Arg	Leu	Asn	Trp	Gln	Ile	Lys	Asp	Leu	Asn	Leu	Phe	
87															180	185	190
89	Tyr	Ser	Phe	Leu	Phe	Cys	Tyr	Leu	Trp	Ser	Val	Pro	Pro	Phe	Leu	Leu	
90															195	200	205
92	Phe	Leu	Val	Ser	Ser	Gly	Met	Leu	Thr	Val	Ser	Leu	Gly	Arg	His	Met	
93															210	215	220
95	Arg	Thr	Met	Lys	Val	Tyr	Thr	Arg	Asn	Ser	Arg	Asp	Pro	Ser	Leu	Glu	
96	225														230	235	240
98	Ala	His	Ile	Lys	Ala	Leu	Lys	Ser	Leu	Val	Ser	Phe	Phe	Cys	Phe	Phe	
99															245	250	255
101	Val	Ile	Ser	Ser	Cys	Val	Ala	Phe	Ile	Ser	Val	Pro	Leu	Ile	Leu		
102															260	265	270
104	Trp	Arg	Asp	Lys	Ile	Gly	Val	Met	Val	Cys	Val	Gly	Ile	Met	Ala	Ala	
105															275	280	285
107	Cys	Pro	Ser	Gly	His	Ala	Ala	Ile	Leu	Ile	Ser	Gly	Asn	Ala	Lys	Leu	
108															290	295	300
110	Arg	Arg	Ala	Val	Met	Thr	Ile	Leu	Leu	Trp	Ala	Gln	Ser	Ser	Leu	Lys	
111	305														310	315	320
113	Val	Arg	Ala	Asp	His	Lys	Ala	Asp	Ser	Arg	Thr	Leu	Cys				
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125	at	ac	at	gc	ag	ct	aat	gg	gt	at	ttt	gg	tt	tt	tt	tt	180
126	tt	cct	tg	at	cc	ca	aa	ttt	cc	at	ttt	cc	tt	tt	tt	tt	240
127	tca	ac	c	cc	ta	at	ttt	tt	t	tc	tt	tt	tt	tt	tt	tt	300
128	at	at	ttt	ttt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	360
129	aa	gat	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	420
130	at	ac	cc	tc	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	tt	480
131	aa	ac	at	tc	gt	gt	tatt	g	ta	ac	tt	tc	tc	tc	tc	tc	540
132	aa	aa	aa	aa	aa	aa	aa	aa	aa	aa	aa	aa	aa	aa	aa	aa	600
133	gt	g	ac	t	c	c	t	c	t	c	t	c	t	c	t	c	660

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134 cacaccctac acatgggaag caatgccaca gggtccaacg accccagcat ggaggctcac 720
 135 atgggggcca tcaaagctat cagctactt ctcattctct acatttcaa tgcagttgt 780
 136 ctgtttatct acctgtccaa catgttgcac atcaacagtc tgtgaaataa tttgtccag 840
 137 atcatcatgg ctgcctaccc tgccagccac tcaattctac tgattcaaga taaccctggg 900
 138 ctgagaagag cctggaagcg gcttcagctt cgacttcatac tttacccaaa agagtggact 960
 139 ctgtga 966
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 143 <211> LENGTH: 321
 144 <212> TYPE: PRT
 145 <213> ORGANISM: Homo sapiens
 147 <400> SEQUENCE: 4
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 151 Ile Thr Leu Ile Leu Ala Val Leu Leu Ala Glu Tyr Leu Ile Gly Ile
 152 20 25 30
 154 Ile Ala Asn Gly Phe Ile Met Ala Ile His Ala Ala Glu Trp Val Gln
 155 35 40 45
 157 Asn Lys Ala Val Ser Thr Ser Gly Arg Ile Leu Val Phe Leu Ser Val
 158 50 55 60
 160 Ser Arg Ile Ala Leu Gln Ser Leu Met Met Leu Glu Ile Thr Ile Ser
 161 65 70 75 80
 163 Ser Thr Ser Leu Ser Phe Tyr Ser Glu Asp Ala Val Tyr Tyr Ala Phe
 164 85 90 95
 166 Lys Ile Ser Phe Ile Phe Leu Asn Phe Cys Ser Leu Trp Phe Ala Ala
 167 100 105 110
 169 Trp Leu Ser Phe Phe Tyr Phe Val Lys Ile Ala Asn Phe Ser Tyr Pro
 170 115 120 125
 172 Leu Phe Leu Lys Leu Arg Trp Arg Ile Thr Gly Leu Ile Pro Trp Leu
 173 130 135 140
 175 Leu Trp Leu Ser Val Phe Ile Ser Phe Ser His Ser Met Phe Cys Ile
 176 145 150 155 160
 178 Asn Ile Cys Thr Val Tyr Cys Asn Asn Ser Phe Pro Ile His Ser Ser
 179 165 170 175
 181 Asn Ser Thr Lys Lys Thr Tyr Leu Ser Glu Ile Asn Val Val Gly Leu
 182 180 185 190
 184 Ala Phe Phe Asn Leu Gly Ile Val Thr Pro Leu Ile Met Phe Ile
 185 195 200 205
 187 Leu Thr Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr Leu His
 188 210 215 220
 190 Met Gly Ser Asn Ala Thr Gly Ser Asn Asp Pro Ser Met Glu Ala His
 191 225 230 235 240
 193 Met Gly Ala Ile Lys Ala Ile Ser Tyr Phe Leu Ile Leu Tyr Ile Phe
 194 245 250 255
 196 Asn Ala Val Ala Leu Phe Ile Tyr Leu Ser Asn Met Phe Asp Ile Asn
 197 260 265 270
 199 Ser Leu Trp Asn Asn Leu Cys Gln Ile Ile Met Ala Ala Tyr Pro Ala
 200 275 280 285
 202 Ser His Ser Ile Leu Leu Ile Gln Asp Asn Pro Gly Leu Arg Arg Ala
 203 290 295 300

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205 Trp Lys Arg Leu Gln Leu Arg Leu His Leu Tyr Pro Lys Glu Trp Thr
206 305 310 315 320
208 Leu
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213 <211> LENGTH: 972
214 <212> TYPE: DNA
215 <213> ORGANISM: Homo sapiens
217 <400> SEQUENCE: 5
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219 actttgggtgg tctccggaat agagtgcatac actggcatcc ttgggagttgg ctccatcactg 120
220 gccatctatg gggtcgatgt ggcaggggc aaaacactcc ccactggtga ccgcattatg 180
221 ttgtatgttgc gctttccag gcttgcata cagatttggta tgatgtgttgc gaacatttgc 240
222 aatctgttatc tccgaatttgt ttataaccat aactcagtgt atatcctctt caaagtcatc 300
223 actgtcttgc tgaaccattc caatctctgg tttgtgcctt ggctcaaagt cttctattgt 360
224 ctttagaatttgc caaacttcaa tcatttcatttgc ttcttcatttgc tgaagaggaa aatcatatgt 420
225 ctgtatgcctt ggcttctcag gctgtcagtg ttgggttcctt taagcttcag ctttccctc 480
226 tcgagagatg tcttcaatgt gtatgtgaat agctccattc ctatccctc ctccaaactcc 540
227 aegggagaaga agtacttctc tgagaccaat atggtaacc tggattttt ctataacatg 600
228 gggatcttcg ttcctctgtat catgttccatc ctggcagccca ccctgtgtat cctctctc 660
229 aagagacaca ccctacacat gggaaagcaat gcccacagggt ccaggaccc cagcatgaag 720
230 gtcacatag gggccatcaa agccaccagg tactttctca tcctctacat tttcaatgca 780
231 attgtcttat ttcttccac gtccaaatc tttgacactt acagttctgtt gaatattttg 840
232 tqcaagatca tcattggctgc ctaccctgcc ggccactcag tacaactgat cttgggcaac 900
233 cctggctgtga gaagacccgtt gaagcggtt cagcaccaag ttccttta cctaaaagg 960
234 cagactctgtt ga 972
237 <210> SEQ ID NO: 6
238 <211> LENGTH: 323
239 <212> TYPE: PRT
240 <213> ORGANISM: Homo sapiens
242 <400> SEQUENCE: 6
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246 Lys Val Thr Phe Thr Leu Val Val Ser Gly Ile Glu Cys Ile Thr Gly
247 20 25 30
249 Ile Leu Gly Ser Gly Phe Ile Thr Ala Ile Tyr Gly Ala Glu Trp Ala
250 35 40 45
252 Arg Gly Lys Thr Leu Pro Thr Gly Asp Arg Ile Met Leu Met Leu Ser
253 50 55 60
255 Phe Ser Arg Leu Leu Gln Ile Trp Met Met Leu Glu Asn Ile Phe
256 65 70 75 80
258 Ser Leu Leu Phe Arg Ile Val Tyr Asn Gln Asn Ser Val Tyr Ile Leu
259 85 90 95
261 Phe Lys Val Ile Thr Val Phe Leu Asn His Ser Asn Leu Trp Phe Ala
262 100 105 110
264 Ala Trp Leu Lys Val Phe Tyr Cys Leu Arg Ile Ala Asn Phe Asn His
265 115 120 125
267 Pro Leu Phe Phe Leu Met Lys Arg Lys Ile Ile Val Leu Met Pro Trp
268 130 135 140
270 Leu Leu Arg Leu Ser Val Leu Val Ser Leu Ser Phe Ser Phe Pro Leu

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271 145 150 155 160
 273 Ser Arg Asp Val Phe Asn Val Tyr Val Asn Ser Ser Ile Pro Ile Pro
 274 165 170 175
 276 Ser Ser Asn Ser Thr Glu Lys Lys Tyr Phe Ser Glu Thr Asn Met Val
 277 180 185 190
 279 Asn Leu Val Phe Phe Tyr Asn Met Gly Ile Phe Val Pro Leu Ile Met
 280 195 200 205
 282 Phe Ile Leu Ala Ala Thr Leu Leu Ile Leu Ser Leu Lys Arg His Thr
 283 210 215 220
 285 Leu His Met Gly Ser Asn Ala Thr Gly Ser Arg Asp Pro Ser Met Lys
 286 225 230 235 240
 288 Ala His Ile Gly Ala Ile Lys Ala Thr Ser Tyr Phe Leu Ile Leu Tyr
 289 245 250 255
 291 Ile Phe Asn Ala Ile Ala Leu Phe Leu Ser Thr Ser Asn Ile Phe Asp
 292 260 265 270
 294 Thr Tyr Ser Ser Trp Asn Ile Leu Cys Lys Ile Ile Met Ala Ala Tyr
 295 275 280 285
 297 Pro Ala Gly His Ser Val Gln Leu Ile Leu Gly Asn Pro Gly Leu Arg
 298 290 295 300
 300 Arg Ala Trp Lys Arg Phe Gln His Gln Val Pro Leu Tyr Leu Lys Gly
 301 305 310 315 320
 303 Gln Thr Leu
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 308 <211> LENGTH: 930
 309 <212> TYPE: DNA
 310 <213> ORGANISM: Homo sapiens
 312 <400> SEQUENCE: 7
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 315 atctccctttg ctgaccaaattt ttcactgtctt ctggcggtctt ccagagttgg tttgtctgg 180
 316 gtattattat taaactggta ttcaactgtt ttgaatccag cttttaatag tgtagaagta 240
 317 agaactactg cttataatat ctgggcagtg atcaaccattt tcagcaactg gcttgctact 300
 318 accctcagca tatttttattt gctcaagattt gccaattttt ccaactttat ttttcttcac 360
 319 ttaaagagga gagttaaagag tgcattctg gtgtatgtt tggggcctt gctattttt 420
 320 gcttgcattt ttttgcattt aaacatgaat gagattgtgc ggacaaaaga atttgaagga 480
 321 aacatgactt ggaagatcaa attgaagagt gcaatgtact tttcaaatat gactgtaacc 540
 322 atggtagcaa acttagtacc cttcactctg accctactat ttttatgtt gttaatctgt 600
 323 tctttgttta aacatctcaa gaagatgcag ctccatggta aaggatctca agatcccagc 660
 324 accaagggtcc acataaaaagc ttgcacaaact gtgtatcttctt tcccttgcattt atgtgccatt 720
 325 tactttctgtt ccataatgtt atcagtttg agttttggaa gtctggaaaa caaacctgtc 780
 326 ttcatgttctt gcaaagctat tagattcagc tatttttcaaa tccacccattt catcctgattt 840
 327 tggggaaaaca agaagctaaa gcagactttt ctgcattttt tttggcaaat gaggtactgg 900
 328 gtgaaaggag agaagacttc atctccatag 930
 331 <210> SEQ ID NO: 8
 332 <211> LENGTH: 309
 333 <212> TYPE: PRT
 334 <213> ORGANISM: Homo sapiens
 336 <400> SEQUENCE: 8
 337 Met Ile Thr Phe Leu Pro Ile Phe Ser Ser Leu Val Val Val Thr

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa

VERIFICATION SUMMARY

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L:1121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1222 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1367 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30